

IN THE CLAIMS

The status of each claim is provided below.

Claims 1-128: Canceled.

129. (New) An isolated DNA sequence encoding a cdc27 protein,
wherein the protein comprises a NH₂-terminal domain conserved in cdc27
homologues of different origin, wherein the NH₂-terminal domain comprises a stretch of 161
NH₂-terminal amino acids, and wherein the stretch comprises SEQ ID NO: 6 or an amino
acid sequence having at least 50% sequence identity to SEQ ID NO: 6,
wherein the protein contains an intact tetratricopeptide domain, and
wherein the protein is capable of modulating DNA replication in plant cells.

130. (New) The DNA sequence of Claim 129, wherein the protein promotes
anaphase promoting complex-substrate action.

131. (New) The DNA sequence of Claim 129, wherein the stretch comprises SEQ ID
NO: 6.

132. (New) The DNA sequence of Claim 129, wherein the stretch comprises an
amino acid sequence having at least 60% sequence identity to SEQ ID NO: 6.

133. (New) The DNA sequence of Claim 129, wherein the stretch comprises an
amino acid sequence having at least 70% sequence identity to SEQ ID NO: 6.

134. (New) The DNA sequence of Claim 129, wherein the stretch comprises an amino acid sequence having at least 80% sequence identity to SEQ ID NO: 6.

135. (New) The DNA sequence of Claim 129, wherein the stretch comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6.

136. (New) The DNA sequence of Claim 129, wherein the stretch comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6.

137. (New) The DNA sequence of Claim 129, wherein the stretch comprises an amino acid sequence having at least 98% sequence identity to SEQ ID NO: 6.

138. (New) The DNA sequence of Claim 129, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 has at least 75% homology to nucleotides 109-181 of SEQ ID NO: 9.

139. (New) The DNA sequence of Claim 129, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 has at least 80% homology to nucleotides 109-181 of SEQ ID NO: 9.

140. (New) The DNA sequence of Claim 129, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence

identity to SEQ ID NO: 6 has at least 90% homology to nucleotides 109-181 of SEQ ID NO: 9.

141. (New) The DNA sequence of Claim 129, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 has at least 95% homology to nucleotides 109-181 of SEQ ID NO: 9.

142. (New) The DNA sequence of Claim 129, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 is nucleotides 109-181 of SEQ ID NO: 9.

143. (New) The DNA sequence of Claim 129, which is in the form of a vector.

144. (New) The DNA sequence of Claim 143, wherein the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

145. (New) The DNA sequence of Claim 143, wherein the vector comprises a nematode-induced promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

146. (New) A method of modulating plant cell division, comprising transforming plant cells with the isolated DNA of Claim 129.

147. (New) The method of Claim 146, wherein the DNA sequence is in the form of a vector, and the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

148. (New) A method of modulating the growth of plant cells, comprising transforming plant cells with the isolated DNA of Claim 129.

149. (New) The method of Claim 148, wherein the DNA sequence is in the form of a vector, and the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

150. (New) A method of modulating DNA replication in plant cells, comprising transforming plant cells with the isolated DNA sequence of Claim 129.

151. (New) The method of Claim 150, wherein the DNA sequence is in the form of a vector, and the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

152. (New) A method of producing transgenic plant cells, comprising transforming plant cells with the isolated DNA of Claim 129.

153. (New) The method of Claim 152, wherein the DNA sequence is in the form of a vector, and the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

154. (New) The method of Claim 153, further comprising:
culturing the plant cells in order to regenerate plant parts or plants from the transformed cells cells, or
incubating the cells at conditions allowing expression of said DNA to produce said protein.

155. (New) A method of producing transgenic plants, comprising transforming plants with the isolated DNA sequence of Claim 129.

156. (New) The method of Claim 155, wherein the protein promotes anaphase promoting complex-substrate action and allows DNA replication.

157. (New) The method of Claim 155, wherein the stretch comprises SEQ ID NO: 6.

158. (New) The method of Claim 155, wherein the stretch comprises an amino acid sequence having at least 60% sequence identity to SEQ ID NO: 6.

159. (New) The method of Claim 155, wherein the stretch comprises an amino acid sequence having at least 70% sequence identity to SEQ ID NO: 6.

160. (New) The method of Claim 155, wherein the stretch comprises an amino acid sequence having at least 80% sequence identity to SEQ ID NO: 6.

161. (New) The method of Claim 155, wherein the stretch comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6.

162. (New) The method of Claim 155, wherein the stretch comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6.

163. (New) The method of Claim 155, wherein the stretch comprises an amino acid sequence having at least 98% sequence identity to SEQ ID NO: 6.

164. (New) The method of Claim 155, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 has at least 75% homology to nucleotides 109-181 of SEQ ID NO: 9.

165. (New) The method of Claim 155, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 has at least 80% homology to nucleotides 109-181 of SEQ ID NO: 9.

166. (New) The method of Claim 155, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 has at least 90% homology to nucleotides 109-181 of SEQ ID NO: 9.

167. (New) The method of Claim 155, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence

identity to SEQ ID NO: 6 has at least 95% homology to nucleotides 109-181 of SEQ ID NO: 9.

168. (New) The method of Claim 155, wherein the sequence which codes for the stretch comprises SEQ ID NO: 6 or an amino acid sequence having at least 50% sequence identity to SEQ ID NO: 6 is nucleotides 109-181 of SEQ ID NO: 9.

169. (New) The method of Claim 155, wherein the DNA sequence is in the form of a vector.

170. (New) The method of Claim 169, wherein the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

171. (New) The method of Claim 169, wherein the vector comprises a nematode-induced promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

172. (New) A method of producing transgenic plant tissue, comprising transforming plant tissue with the isolated DNA sequence of Claim 129.

173. (New) The method of Claim 172, wherein the DNA sequence is in the form of a vector, and the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

174. (New) A method of modifying the characteristics of plants, comprising transforming plants with the isolated DNA sequence of Claim 129.

175. (New) The method of Claim 174, wherein the DNA sequence is in the form of a vector, and the vector further comprises a promoter operably linked to the DNA, wherein the promoter is functional in plant cells.

176. (New) A plant cell transformed with the DNA sequence of Claim 129.

177. (New) A plant transformed with the DNA sequence of Claim 129.

178. (New) A progeny of the plant of Claim 177, wherein the progeny comprises the DNA sequence which transformed the plant.

179. (New) A plant cell transformed with the vector of Claim 143.

180. (New) A plant transformed with the vector of Claim 143.

181. (New) A progeny of the plant of Claim 180, wherein the progeny comprises the DNA sequence which transformed the plant.

182. (New) A plant material obtained from the plant of Claim 181, wherein the plant material comprises the vector which transformed the plant.

183. (New) The plant material of Claim 182, which is one or more selected from the group consisting of roots, flowers, fruit, leaves, pollen, seeds, seedlings and tubers.

184. (New) A plant material obtained from the plant of Claim 180, wherein the plant material comprises the vector which transformed the plant.

185. (New) The plant material of Claim 184, which is one or more selected from the group consisting of roots, flowers, fruit, leaves, pollen, seeds, seedlings and tubers.

186. (New) A plant cell obtained by the method of Claim 146.

187. (New) A plant cell obtained by the method of Claim 147.

188. (New) A plant cell obtained by the method of Claim 148.

189. (New) A plant cell obtained by the method of Claim 149.

190. (New) A plant cell obtained by the method of Claim 150.

191. (New) A plant cell obtained by the method of Claim 151.

192. (New) A plant cell obtained by the method of Claim 152.

193. (New) A plant cell obtained by the method of Claim 153.

- 194. (New) A plant cell obtained by the method of Claim 154.
- 195. (New) A plant obtained by the method of Claim 155.
- 196. (New) A plant obtained by the method of Claim 156.
- 197. (New) A plant obtained by the method of Claim 157.
- 198. (New) A plant obtained by the method of Claim 158.
- 199. (New) A plant obtained by the method of Claim 159.
- 200. (New) A plant obtained by the method of Claim 160.
- 201. (New) A plant obtained by the method of Claim 161.
- 202. (New) A plant obtained by the method of Claim 162.
- 203. (New) A plant obtained by the method of Claim 163.
- 204. (New) A plant obtained by the method of Claim 164.
- 205. (New) A plant obtained by the method of Claim 165.
- 206. (New) A plant obtained by the method of Claim 166.

- 207. (New) A plant obtained by the method of Claim 167.
- 208. (New) A plant obtained by the method of Claim 168.
- 209. (New) A plant obtained by the method of Claim 169.
- 210. (New) A plant obtained by the method of Claim 170.
- 211. (New) A plant obtained by the method of Claim 171.
- 212. (New) A plant tissue obtained by the method of Claim 172.
- 213. (New) A plant tissue obtained by the method of Claim 173.
- 214. (New) A plant obtained by the method of Claim 174.
- 215. (New) A plant obtained by the method of Claim 175.

SUPPORT FOR THE AMENDMENTS

Claims 29-128 have been cancelled in favor of Claims 129-215. Newly-added Claims 129-215 are supported by the specification and the original claims. In particular, Claim 129 is supported by the specification at paragraph [0021] which states that “SEQ ID NO: 6, and thus also SEQ ID NO: 10, are part of a unique NH₂-terminal domain conserved in CDC27 homologues of different origin.” SEQ ID NO: 10 is in fact the stretch of 161 NH₂-terminal amino acids recited in Claim 129. Similarly, paragraph [0017] states “The novel exon encoded by amino acid sequence SEQ ID NO: 6 [sequence omitted] is part of a unique NH₂-terminal domain conserved in CDC27 homologues of different origin.” Reference to sequences having at least 50% identity to SEQ ID NO: 6 may be found in, for example, paragraph [0009]. Thus, there is ample support in the application as filed for an NH₂-terminal domain conserved in cdc27 homologues of different origin comprising a stretch of 161 NH₂-terminal amino acids and comprising SEQ ID NO: 6 or a sequence having at least 50% identity thereto. Accordingly, no new matter is believed to be added to the present application by the amendments submitted above.